

FIG. 1A

Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu Ala Leu Ser His
1 5 10 15
Thr Ala Asn Pro Cys Cys Ser His Pro Cys Gln Asn Arg Gly Val Cys
20 25 30
Met Ser Val Gly Phe Asp Gln Tyr Lys Cys Asp Cys Thr Arg Thr Gly
35 40 45
Phe Tyr Gly Glu Asn Cys Ser Thr Pro Glu Phe Leu Thr Arg Ile Lys
50 55 60
Leu Phe Leu Lys Pro Thr Pro Asn Thr Val His Tyr Ile Leu Thr His
65 70 75 80
Phe Lys Gly Phe Trp Asn Val Val Asn Asn Ile Pro Phe Leu Arg Asn
85 90 95
Ala Ile Met Ser Tyr Val Leu Thr Ser Arg Ser His Leu Ile Asp Ser
100 105 110
Pro Pro Thr Tyr Asn Ala Asp Tyr Gly Tyr Lys Ser Trp Glu Ala Phe
115 120 125
Ser Asn Leu Ser Tyr Tyr Thr Arg Ala Leu Pro Pro Val Pro Asp Asp
130 135 140
Cys Pro Thr Pro Leu Gly Val Lys Gly Lys Lys Gln Leu Pro Asp Ser
145 150 155 160
Asn Glu Ile Val Glu Lys Leu Leu Leu Arg Arg Lys Phe Ile Pro Asp
165 170 175
Pro Gln Gly Ser Asn Met Met Phe Ala Phe Phe Ala Gln His Phe Thr
180 185 190
His Gln Phe Phe Lys Thr Asp His Lys Arg Gly Pro Ala Phe Thr Asn
195 200 205
Gly Leu Gly His Gly Val Asp Leu Asn His Ile Tyr Gly Glu Thr Leu
210 215 220
Ala Arg Gln Arg Lys Leu Arg Leu Phe Lys Asp Gly Lys Met Lys Tyr
225 230 235 240
Gln Ile Ile Asp Gly Glu Met Tyr Pro Pro Thr Val Lys Asp Thr Gln
245 250 255
Ala Glu Met Ile Tyr Pro Pro Gln Val Pro Glu His Leu Arg Phe Ala
260 265 270
Val Gly Gln Glu Val Phe Gly Leu Val Pro Gly Leu Met Met Tyr Ala
275 280 285
Thr Ile Trp Leu Arg Glu His Asn Arg Val Cys Asp Val Leu Lys Gln
290 295 300

FIG. 1B

Glu His Pro Glu Trp Gly Asp Glu Gln Leu Phe Gln Thr Ser Arg Leu
305 310 315 320

Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Asp Tyr Val Gln
325 330 335

His Leu Ser Gly Tyr His Phe Lys Leu Lys Phe Asp Pro Glu Leu Leu
340 345 350

Phe Asn Lys Gln Phe Gln Tyr Gln Asn Arg Ile Ala Ala Glu Phe Asn
355 360 365

Thr Leu Tyr His Trp His Pro Leu Leu Pro Asp Thr Phe Gln Ile His
370 375 380

Asp Gln Lys Tyr Asn Tyr Gln Gln Phe Ile Tyr Asn Asn Ser Ile Leu
385 390 395 400

Leu Glu His Gly Ile Thr Gln Phe Val Glu Ser Phe Thr Arg Gln Ile
405 410 415

Ala Gly Arg Val Ala Gly Gly Arg Asn Val Pro Pro Ala Val Gln Lys
420 425 430

Val Ser Gln Ala Ser Ile Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser
435 440 445

Phe Asn Glu Tyr Arg Lys Arg Phe Met Leu Lys Pro Tyr Glu Ser Phe
450 455 460

Glu Glu Leu Thr Gly Glu Lys Glu Met Ser Ala Glu Leu Glu Ala Leu
465 470 475 480

Tyr Gly Asp Ile Asp Ala Val Glu Leu Tyr Pro Ala Leu Leu Val Glu
485 490 495

Lys Pro Arg Pro Asp Ala Ile Phe Gly Glu Thr Met Val Glu Val Gly
500 505 510

Ala Pro Phe Ser Leu Lys Gly Leu Met Gly Asn Val Ile Cys Ser Pro
515 520 525

Ala Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Gln Ile
530 535 540

Ile Asn Thr Ala Ser Ile Gln Ser Leu Ile Cys Asn Asn Val Lys Gly
545 550 555 560

Cys Pro Phe Thr Ser Phe Ser Val Pro Asp Pro Glu Leu Ile Lys Thr
565 570 575

Val Thr Ile Asn Ala Ser Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn
580 585 590

Pro Thr Val Leu Leu Lys Glu Arg Ser Thr Glu Leu
595 600

FIG. 2A

GTCCAGGAAC TCCTCAGCAG CGCTCCTTC AGCTCCACAG CCAGACGCCC TCAGACAGCA 60
AAGCCTACCC CCGCGCCGCG CCCTGCCCGC CGCTGCGATG CTCGCCCGCG CCCTGCTGCT 120
GTGGCGGGTC CTGGCGCTCA GCCATACAGC AAATCCTTGC TGTTCACACC CATGTCAAAA 180
CCGAGGTGTA TGTATGAGTG TGGGATTGTA CCAGTATAAG TCGATTGTA CCCGGACAGG 240
ATTCTATGGA GAAAACTGCT CAACACCGGA ATTTTIGACA AGAATAAAAT TA'TTCTGAA 300
ACCCACTCCA AACACAGTGC ACTACATACT TACCCACTTC AAGGGATTIT GGAACGTTGT 360
GAATAACATT CCCTTCCTTC GAAATGCAAT TATGAGTTAT GTGTTGACAT CCAGATCACA 420
TTTGATTGAC AGTCCACCAA CTTACAATGC TGACTATGGC TACAAAAGCT GGGAAGCCTT 480
CTCTAACCTC TCCTATTATA CTAGAGCCCT TCCTCCTGTG CCTGATGATT GCCCGACTCC 540
CTTGGGTGTC AAAGGTAAAA AGCAGCTTCC TGATTCAAAT GAGATTGTGG AAAAAATTGCT 600
TCTAAGAAGA AAGTTCATCC CTGATCCCA GGGCTCAAAC ATGATGTTTG CATTCTTTGC 660
CCAGCACTTC ACGCACCAGT TTTCAAGAC AGATCATAAG CGAGGGCCAG CTTTCACCAA 720
CGGGCTGGGC CATGGGTGG ACTTAAATCA TATTTACGGT GAAACTCTGG CTAGACAGCG 780
TAAACTGCGC CTTTCAAGG ATGGAAAAAT GAAATATCAG ATAATTGATG GAGAGATGTA 840
TCCTCCACA GTCAAAGATA CTCAGGCAGA GATGATCTAC CCTCCTCAAG TCCCTGAGCA 900
TCTACGGTTT GCTGTGGGGC AGGAGGTCTT TGGTCTGGTG CCTGGTCTGA TGATGTATGC 960
CACAATCTOG CTGCGGGAAC ACAACAGAGT ATGTGATGTG CTTAAACAGG AGCATCCTGA 1020
ATGGGGTGAT GAGCAOTTGT TCCAGACAAG CAGGCTAATA CTGATAGGAG AGACTATTAA 1080
GATTGTGATT GAAGATTATG TGCAACACTT GAGTGGCTAT CACTTCAAAC TGAAATTTGA 1140
CCCAGAACTA CTTTCAACA AACAATTCCA GTACCAAAAT CGTATTGCTG CTGAATTTAA 1200
CACCTCTAT CACTGGCATC CCCTTCTGCC TGACACCTT CAAATTCATG ACCAGAAATA 1260
CAACTATCAA CAGTTTATCT ACAACAATC TATATTGCTG GAACATGGAA TTACCCAGTT 1320
TGTGAATCA TTCACCAGGC AAATTGCTGG CAGGGTTGCT GGTGGTAGGA ATGTCCACC 1380
CGCAGTACAG AAATATCAC AGGCTTCCAT TGACCAGAGC AGGCAGATGA AATACCAGTC 1440
TTTAAATGAG TACCGCAAAC GCTTTATGCT GAAGCCCTAT GAATCATTG AAGAACTTAC 1500
AGGAGAAAAG GAAATGTCTG CAGATTGGA AGCACTCTAT GGTGACATCG ATGCTGTGGA 1560
GCTGTATCCT GCCCTTCTGG TAGAAAAGCC TCGCCAGAT GCCATCTTTG GTGAAACCAT 1620
GGTAGAAGTT GGAGCACCAT TCTCCTGAA AGGACTTATG GGTAAATGTA TATGTTCTCC 1680
TGCTACTGG AAGCCAAGCA CTTTGGTGG AGAAGTGGGT TTCAAATCA TCAACACTGC 1740

FIG. 2B

CTCAATTCAG TCTCTCATCT GCAATAACGT GAAGGGCTGT CCCTTTACTT CATTCAGTGT	1800
TCCAGATCCA GAGCTCATTA AAACAGTCAC CATCAATGCA AGTTCTTCCC GCTCCGGAAT	1860
AGATGATATC AATCCACAG TACTACTAAA AGAACGGTCG ACTGAACTGT AGAAGTCTA	1920
TGATCATATT TATTTATTTA TATGAACCAT GTCTATTAAT TTAATTATTT AATAATATTT	1980
ATATTAAGCT CCTTATGTTA CTTAACATCT TCTGTAACAG AAGTCAGTAC TCCTGTTGCC	2040
GAGAAAGGAG TCATACTTGT GAAGACTTTT ATGTCAGTAC TCTAAAGATT TTGCTGTTGC	2100
TGTTAAGTTT GGAAAACAGT TTTTATTCTG TTTTATAAAC CAGAGAGAAA TGAGTTTTGA	2160
CGTCTTTTTC CTTGAATTTT AACTTATATT ATAAGGACGA AAGTAAAGAT GTTTGAATAC	2220
TAAACACTA TCACAAGATG CCAAAATGCT GAAAGTTTTT AACTGTTCGA TGTTTCCAAT	2280
GCATCTTCCA TGATGCATTA GAAGTAACTA ATGTTTGAAA TTTTAAAGTA CTTTGGGTA	2340
TTTTCTGTC ATCAAACAAA ACAGGTATCA GTGCATTATT AAATGAATAT TTAAATTAGA	2400
CATTACCAGT AATTTCATGT CTACTTTTTC AAATCAGCAA TGAAACAATA ATTTGAAATT	2460
TCTAAATTC TAGGGTAGAA TCACCTGTAA AAGCTTGTTT GATTCTTAA AGTTATTAAA	2520
CTTGACATA TACCAAAAAG AAGCTGTCTT GGATTTAAAT CTGTAAATC AGATGAAATT	2580
TTACTACAAT TGCTTGTTAA AATATTTTAT AAGTGATGTT CCTTTTTCAC CAAGAGTATA	2640
AACCTTTTTC GTGTGACTGT TAAACTTCC TTTTAAATCA AAATGCCAAA TTTATTAAGG	2700
TGGTGGAGCC ACTGCAGTGT TATCTCAAAA TAAGAATATC CTGTTGAGAT ATCCAGAAT	2760
CTGTTTATAT GGCTGGTAAC ATGTAAAAAC CCCATAACCC CGCCAAAAGG GGTCCATCCC	2820
TTGAACATAA AGCAATAACC AAAGGAGAAA AGCCCAAATT ATTGGTTCCA AATTTAGGGT	2880
TTAAACTTTT TGAAGCAAAC TTTTTTTTAG CCTGTGTCAC TGCAGACCTG GACTCAGAT	2940
TTTGCTATGA GGTTAATGAA GTACCAAGCT GTGCTTGAAT AACGATATGT TTTCTCAGAT	3000
TTTCTGTTGT ACAGTTTAAAT TTAGCAGTCC ATATCACATT GCAAAAGTAG CAATGACCTC	3060
ATAAAATACC TCTTCAAAAT GCTTAAATTC ATTTACACA TTAATTTTAT CTCAGTCTTG	3120
AAGCCAATTC AGTAGGTGCA TTGGAATCAA GCTGGCTAC CTGCATGCTG TTCCTTTTCT	3180
TTTCTCTTT TAGCCATTTT GCTAAGAGAC ACAGTCTTCT CAAACACTTC GTTCTCCTA	3240
TTTTGTITTA CTAGTTTAA GATCAGAGTT CACTTCTTT GGACTCTGCC TATATTTTCT	3300
TACCTGAACT TTTGCAAGTT TTCAGGTAAA CCTCAGCTCA GGACTGCTAT TTAGCTCCTC	3360
TTAAGAAGAT TAAAAAAGG AAAAAAG	3387